

Applicant: Rachel E. Meyers, et al.

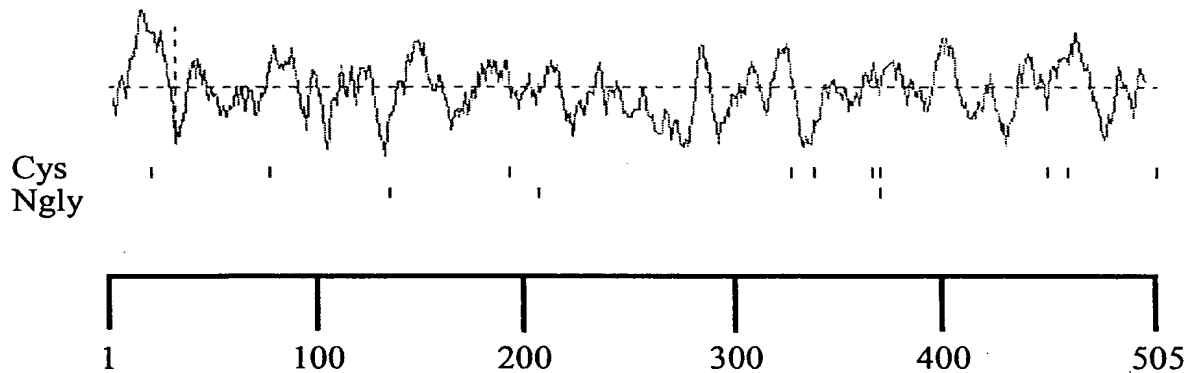
Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES  
THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

Human 33312

Cytochrome p450 Domain



**Fig. 1**

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p450: domain 1 of 1, from 46 to 501: score 400.9, E = 1.2e-116:

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*->PPGPpplPliGnllqlgrapppiphsltklrkakrYgkpvftlylGp
    +P Pp +++ G+ +++ ++ +++++kl + k Y+ ++l++Gp
33312 46  FPAPPAHWFYGHKEFYPV--KEF-EVYHKLME-K-YP-CAVPLWVGP 86

    .rpvVltgpeavkevLidkgeeFakgRgdfnptfpwlsgyreggllfs
    +   +++p+++ +L ++ + ++ + + + w+ g gl+++
33312 87  fTMFFSVHDPDYA-KILLKRQDPKS-AVSHK-ILESWV--GR---GLVTL 128

    dnGpkWrklRrFslltlrfHFgmGa....ysKrsqkleePriqeeardLv
    +G kW+k+R+ + + F + + ++ ++ ++ + + ++
33312 129 -DGSKWKKHRQ--IVKP-G-FNI-SilkiFI-T---MMS-ESVRMMLNKW 167

    erlrkeqagspiDitellarlaplnvicsllF...Gvrfdylrpedpef
    e+ + q +s ++++++++ l+l+ l++++F+++++++d+ D+ +
33312 168 EEHIA-Q-NSRLELFQHS-LMTLDSIMKCAFshqgsIQlds--TLDS-Y 211

    lkldkl1nemfdrvspwhqlldifp...fllrylpgs1frkafkaakd.
    lk++ + l +++ + ++ +++ +++ +++ s + ++f ++ +
33312 212 LKAVERN-LSKIS-N-Q---RMNNFLHndLVFKF--SS-QGQIFSKFNQe 252

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Fig. 2A

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Docket No.: MPI02-107CN1M

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lkdyldklierretlepagdpRrLD.i.....gfldslleakreggnp
l+++++k+i++r+e+l+ + D++++++ +fld+ Ll ak e+
33312 253 LHQFTEKVIQDRKESLKD-KLKQ--DtTqkrrwDFLDI-LLSAKSENT-- 296

kselSdeelaatvldllfAGteTTsstLswaLyllLakhPevqaklreEid
+ +s+ +l a+v +++fAG++TTss++sw+Ly Lak+Pe+q+++r Ei
33312 297 -KDFSEADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQRCRDEIR 345

eviGrdrsptydvDaraqmPYLdAvIkEtLRlypvvPlllprvatkDtei
e +G+++s+t++ + ++qmpY++++Ike LRly +v ++ R + k+++++
33312 346 ELLGDGSSITWE-H-LSQMPYTTMCiKECLRLYAPV-VNISRLLDKPITF 392

pdGylIPKGtlVivnlyslhrDpkvfpnPeeFdPeRFLdengkfksyaf
pdG+ +P+G +V++n++++lh++p +++++P++F+p RF+ en + ++yaf
33312 393 PDGRSLPAGITVFINIwALHhNPYFWEDPQVFNPFRFSRENSekiHPYAF 442

lPFGaGpRnClGerlArmElflflatlLqrFPelelavppgdipsltpkp
+PF+aG RnC+G+++A+ E +++++a+ L rF +l +++++ +p +p +
33312 443 IPFSAGLRNCIGQHFAIIECKVAVALTLRF-KLA--PDHSRPP--QPVR 487

elglpskpplykvqlrpa<-* (SEQ ID NO:10)
+++l sk+++++ + a
33312 488 QVVLKSKNGIH---VF-A 501

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Fig. 2B

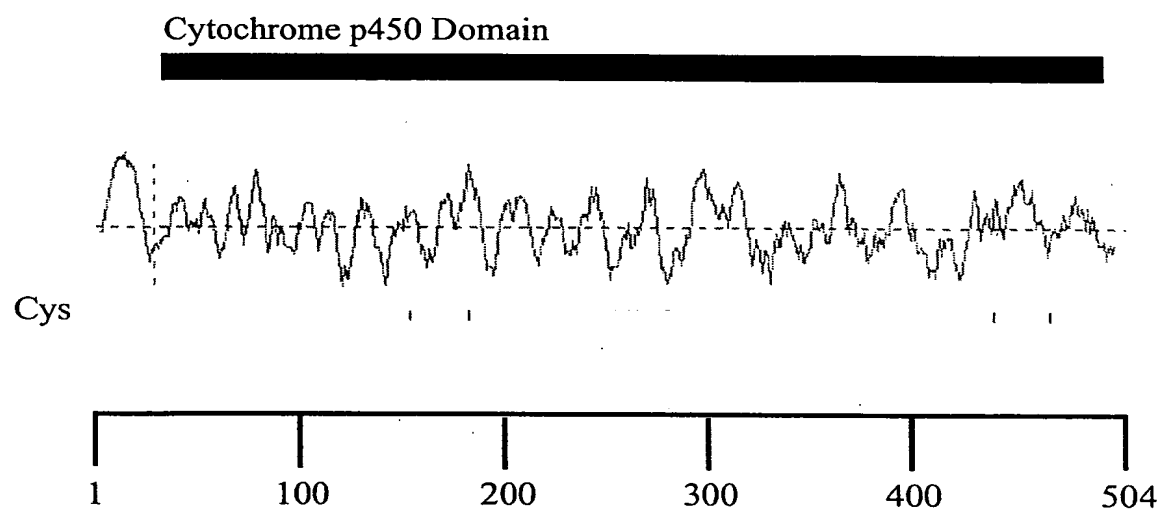
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Human 33303



**Fig. 3**

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## p450: domain 1 of 1, from 33 to 493: score 594.5, E = 6.4e-175:

```

*->PPgPpplPliGnllqlgrappipph.sltklrkkrYgkpvftlylG
  PPGP+plPl+Gnllql+  g + ++ l++l+k k YG pvft+ylg
33303 33  PPGPTPLPLIGNLLQLRP--GAL-YsGLMRLSK-K-YG-PVFTIYLG 73

      p.rpvVvltgpeavkevLldkgeeFakGRgdfnptfpwlsgkyregllf
      p.rpvVv1 g eav+e+l+ +eeF+ gRg +++++ ++g+ g++f
33303 74 PwRPVVVLVGQEAVREALGGQAEFFS-GRGTV-AMLEGTFDGH---GVFF 118

      sdnGpkWrklRrFslltlrHFgmGaysKrsqkleePriqeeardLverl
      s nG++Wr+lR+F++l+lR+ +gmG Kr ee iq ear+Lve++
33303 119 S-NGERWRQLRKFTMLALRD-LGMG---KRE--GEE-LIQAEARCLVETF 160

      rkegagspiDitellarlaplInvIcsllFGvrfdylrpeDpeflklidkl
      + + g p+D++ lla a++nv+csllFG rf Y eD+ef++ ++ +
33303 161 QGTE-GRPFDPSLLLA-QATSNVVCsLLFGLRFSY---EDKEFQAVVR-A 204

      lnemfdrvspwh.qlldiFP.fLlrylpgs1frkafkaakdkldkldli
      +++ vs+ ++q + +f fL++ lpg+ +++++ + l +++++ +
33303 205 AGGTLIGVSSQGgQTYEMFSwFLRP-LPGP-HKQLLHHVSTLAAFTVRQV 252

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Fig. 4A

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eerretlepagdpRrldigfldsllleakreggnpkselsdeelaatvld
++++ l+ g+ R D ++D++ll++ ++ np ++++++ ++tv+
33303 253 QQHQGNLDASGPARG--D--LVDAFLLKMAQEEQNPGTEFTNKNMLMTVIY 298

llfAGteTtsstlswaLyllLakhPevqaklreEideviGrdrsptydvdA
llfAGt T+s+t ++L+ll+k+P+vg+ +reE+ + +G ++ p++ D
33303 299 LLFAGTMTVSTTVGYTLLLLMKYPHVQKWVREELNRELGAGQAPSLG-D- 346

raqmPYLdAvIkEtLRlypvvPlllprvatkDteiPdGylIPKGtlVivn
r ++PY+dAv++E++Rl +vP+++pR++ + t + +Gy++P Gt V++
33303 347 RTRLPYTDAVLHEAQRLLALVPMGIPRTLMTTRF-RGYTL PQGTEVFPL 395

lyslhrDpkvfpnPeeFdPeRFLdengkfksyafLPFGaGpRnClGerl
l+s+++Dp+++f +PeeF+P+RFLd++g+f+k++afLPF+ G+R+ClGe+l
33303 396 LGSILHDPNIFKHPEEFNPDRLDADGRFRKHEAFLPFSLGKRVCLGGL 445

ArmElflflatlLqrFPelelavppgdipsltpkpelglpskpplykvql
A+ Elflf++t+Lq F +le+++pp + l+p + +gl ++pp + ql
33303 446 AKAEFLFFTTILQAF-SLESPCPPDTLS-LKPTV-SGLFNIPPAF--QL 490

rpa<-* (SEQ ID NO:10)
++
33303 491 QVR 493

```

Fig. 4B

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Human 32579

Cytochrome p450 Domain

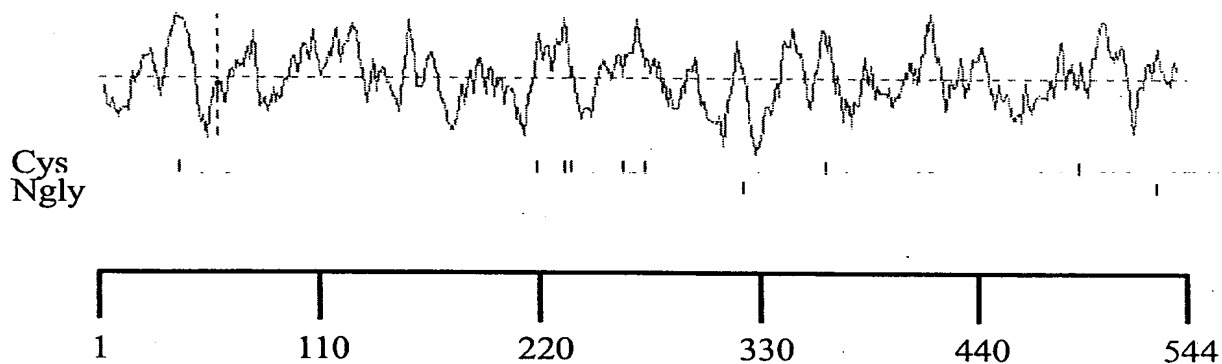


Fig. 5

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Docket No.: MPI02-107CN1M

p450: domain 1 of 2, from 60 to 72: score 7.8, E = 0.21:

\*->PPgPpplPliGnl<-\* (SEQ ID NO:11)

PPgP+p+Pl+Gn+  
32579 60 PPGTPWPLVGNF 72

Fig. 6A

p450: domain 2 of 2, from 107 to 543: score 516.2, E = 2.3e-151:

\*->ltklrkakrYGkpvftlylGprpvVvltgpeavkevLldkgeeeFakg  
1+ 1++ YG ++f++ +G+ vVvl++ v+e+L++++e F+ +  
32579 107 LAHLAR-V-YG-SIFSFFIGHYLVVLSDFHSVREALVQQAEEVFS-D 149  
  
RgdfnptfpwlskgyreqgllfsdnGpkWrklRrFslltlrfHFgmGays  
R++ p +++k + g++f+ +Gp+W++R+Fs+ tlr Fg+G  
32579 150 RPRV-PLISIVTKEK---GVVFAHYGPVWRQQKFSHSTLRH-FGLG--- 191  
  
KrsqkleeePriqeeardLverlrkeqagspiDitellarlaplnvicsll  
K+s le p i ee + +++k++ p+ ++ +++ a++n+Icsl+  
32579 192 KLS--LE-PKIIIEEFKYVKAEMQKHG-EDPFCPFSIIS-NAVSNIICSLC 236  
  
FGvrfdylrpeDpeflklidklldnemfdrv.spwh.qlldiffPfllyl.  
FG rfdy ++ef k++ ++ + ++ + l++i P+L +Yl+  
32579 237 FGQRFDY---TNSEFFKMLG-FMSRGL-EICLNSQVLLVNICPWL-YYLp 280

Fig. 6B



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pgslfrkafkaakd.lkdyldklieerretlepagdpRrldigfldslLl
g+ f+++ ++++++ +l k+i+++++e+l++ +p D f+D Ll
32579 281 FGP-FKELR-QIEKdITSFLKKIIKDQESLDR-ENPQ--D--FIDMYLL 323

eakr.eggnpkxselsdeelaatvldllfAGteTtsstLswaLyLlakhPe
+++++++n +s+++++e l +++dl+++AGT+TT++ L w+L+++ +P+
32579 324 HMEERKNNSNSDFEYLYFYIIGDLFIAGTDTTNSLLWCLLYMSLNPD 373

vqaklreEideviGrdrsptydvDaraqmPYLdAvIkEtLRlypvvPlll
vq+k++eEi+++viG +r p++ D aqmpY++A+I E++Rl vvPl++
32579 374 VQEKVHEEIERVIGANRAPSLT-D-KAQMPTYTEATIMEVQRLTVVPLAI 421

prvatkDteiPdGylIPKGtlVivnlyslhrDpkvfpnPeeFdPeRFLde
p+++++ t++ +Gy+IPKGtl+++nl+s+hrDp+++++Pe F P RFLd
32579 422 PHMTSENTVL-QGYTIPKGTLILPNLWSVHRDPAIWEKPEDFYPNRFLDD 470

ngkfksyaflPFGaGpRnClGerlArmeIfLflLatllqrFPeleleavpp
+g+ k + f+PFG G+R+C Ge+lA+mElfl++ +l+q F + l+ +
32579 471 QGQLIKKETFIPIFGIGKRVCVMGEQLAKMELFLMFVSLMQSF-AFALPEDS 519

gdipsltpkpelglskpplykvqlrpa<-* (SEQ ID NO:12)
+++ lt++ +gl++ p ++++++ +
32579 520 KKPL-LTGR--FGLTLAPHPFNITIS-R 543

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Fig. 6C

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CCCACGGTCCGCCAGAGTGGGGCCGAGGAGGTGTCCGGTCCCGAGCGGGGTTTTTTTTTTCTGCGGGTTGCCTTTTGT
TTTTCTTTGGAACCGCGGTGTGTTCAAAAGCTTGACGGAACCTTGAAGGGGACTCCCACTCTCCTCCCTCTTTCCGCTG

      M D K V C A I F G G S R G I G      15
AGTTTGTGACTCCGAG ATG GAC AAA GTG TGT GCT ATT TTT GGA GGC TCC CGA GGC ATT GGC      45

R A V A Q L M A R K G Y R L A I I A R N      35
AGG GCT GTG GCC CAG TTA ATG GCC CGG AAA GGC TAC CGC CTG GCG ATC ATT GCC AGA AAC      105

L E G A K A A A G D L G G D H L A F S C      55
CTG GAA GGG GOC AAA GCC GCC GCC GGT GAC CTC GGC GGA GAT CAT TTG GCA TTT AGC TGT      165

D V A K E H D V Q N T F E E M E K H L G      75
GAT GTT GCT AAA GAA CAT GAT GTT CAA AAT ACA TTT GAA GAG ATG GAG AAA CAT TTA GGT      225

R V N F L V N A A G I N R D S L L V R T      95
CGA GTA AAT TTC TTG GTA AAT GCA GCT GGT ATT AAC AGG GAT AGT CTT TTA GTA AGA ACA      285

K T E D M V S Q L H T N L L G S M L T C      115
AAA ACT GAA GAT ATG GTA TCT CAG CTT CAT ACT AAC CTC TTG GGT TCC ATG CTG ACC TGT      345

K A A M R A M I Q Q Q G G S I V N V G S      135
AAA GCT GCC ATG AGG GCT ATG ATT CAA CAA CAG GGA GGG TCT ATT GTT AAT GTA GGA AGC      405

I V G L K G N S G Q S V Y S A S K G G L      155
ATT GTT GGC TTA AAA GGC AAC TCT GGC CAG TCC GTT TAC AGT GCC AGT AAA GGA GGA TTA      465

V G F S R A L A K E V A R K K I R V N V      175
GTT GGA TTT TCA CGT GCT CTT GCT AAA GAG GTA GCA AGA AAG AAA ATT AGA GTG AAT GTA      525

V A P G F V H T D M T K D L K E E H L K      195
GTT GCA CCA GGA TTT GTA CAC ACA GAT ATG ACG AAA GAC TTG AAA GAA GAA CAT TTA AAG      585

K N I P L G R F G E T I E V A H A V V F      215
AAA AAT ATT CCT CTT GGG AGG TTT GGA GAA ACT ATT GAG GTG GCA CAT GCG GTT GTG TTT      645

L L E S P Y I T G H V L V V D G G L Q L      235
CTT TTA GAA TCA CCG TAT ATT ACA GGG CAT GTT CTG GTA GTG GAT GGG GGA TTA CAA CTC      705

I L      238
ATT TTG TAA      714

TTTGACAGATTATTACAGTTATAGGGGTGATTAGCATCAAGGGCACACTTTGGCTACTGATTAGACAATTATACCTACATG
GGTAACATGTGCTAATCAAACCTGCTGATGCTACAAATGTTAATTTCTGTCTTTATAAAAAATATGTCTCAAAAGAA

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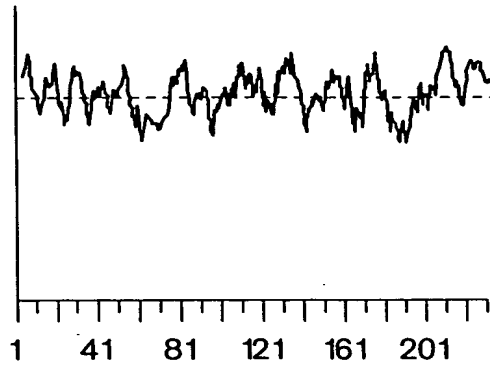
Fig. 7

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THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M



>21509

MDKVCAIFGGSRGIGRAVAQLMARKGYRLAI IARNLEGAKAAAGDLGGDHLAFSCDVAKE  
HDVQNTIFEEMEKHLGRVNFVNAAGINRDSLLVRTKTEDMVSQ LHTNLLGSMLTCKAAMR  
AMIQQQGSIVNVGSIVGLKGNSSQSVYSASKGGLVGF SRALAKEVARKKIRVNVVAPGF  
VHTDMTKDLKEEHLKKNIP LGRFGETIEVAHAVVFLLSPYITGHVLVVDGGLQLIL

Fig. 8

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Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

adh\_short: domain 1 of 1, from 3 to 184: score 217.5, E = 2e-61

```

      *->KvaLvTGassGIGlaiAkrLakeGakVvvadrneeklekGavakelk
      Kv+ + G+s+GIG+a+A+ +a++G+++++rn e +      +++
21509   3      KVCAIFGGSRGIGRAVAQLMARKGYRLAI IARNLEGA-----KAAAG 44

      elGgndkdralaiqlDvtdeesv.aaveqaverlGrlDvLVNNAGgiill
      lGg      la+ +Dv++e +v++++e+ ++lGr++ LVN AG i
21509  45  DLGG----DHLAFSCDVAKEHDVqNTFEEMEKHLGRVNFLVNAAG--I-N 87

      rpgpfaelstneedwdrvidvNltgvfilltravplmamkkrggGrIvN
      r+ + +      ed + +++Nl+g +l+++a+++ am++++gG+IvN
21509  88  RDSLLVVRTK---TEDMVSQLHTNLLGSMLTCKAAMR--AMIQOQGGGSIVN 132

      iSSvaGrkegglvgcpggsaYsASKaAvigltrsLAlElaphgIrVnava
      ++S++G      l+g+ g+s+YsASK++++g++r+LA+E+a+++IrVn+va
21509 133  VGSIVG-----LKGNSGQSVYSASKGGLVGFSRALAKEVARKKIRVNVVA 177

      PGgvdTd<-*
      PG+v Td
21509 178  PGFVHTD      184

```

Fig. 9A

adh\_short\_C2: domain 1 of 1, from 201 to 229: score 29.6, E = 1.1e-06

```

      *->gRlGePeEiAnavvFLASdaAsYiTGqtlvV<-*
      gR+Ge+ E+A avvFL  ++ YiTG++lvV
21509 201  GRFGETIEVAHAVVFL--ESFYITGHVLV  229

```

Fig. 9B

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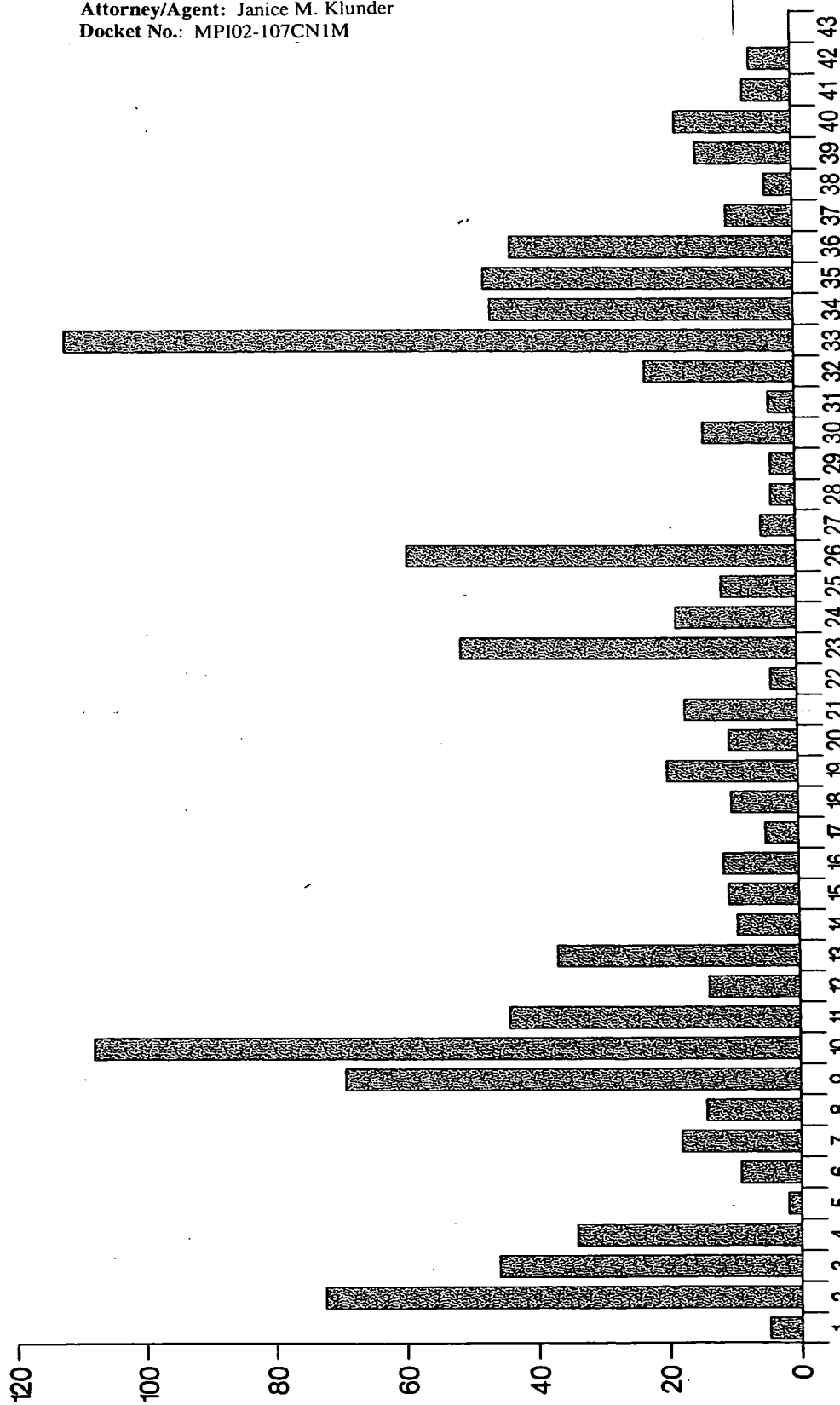


Fig. 10

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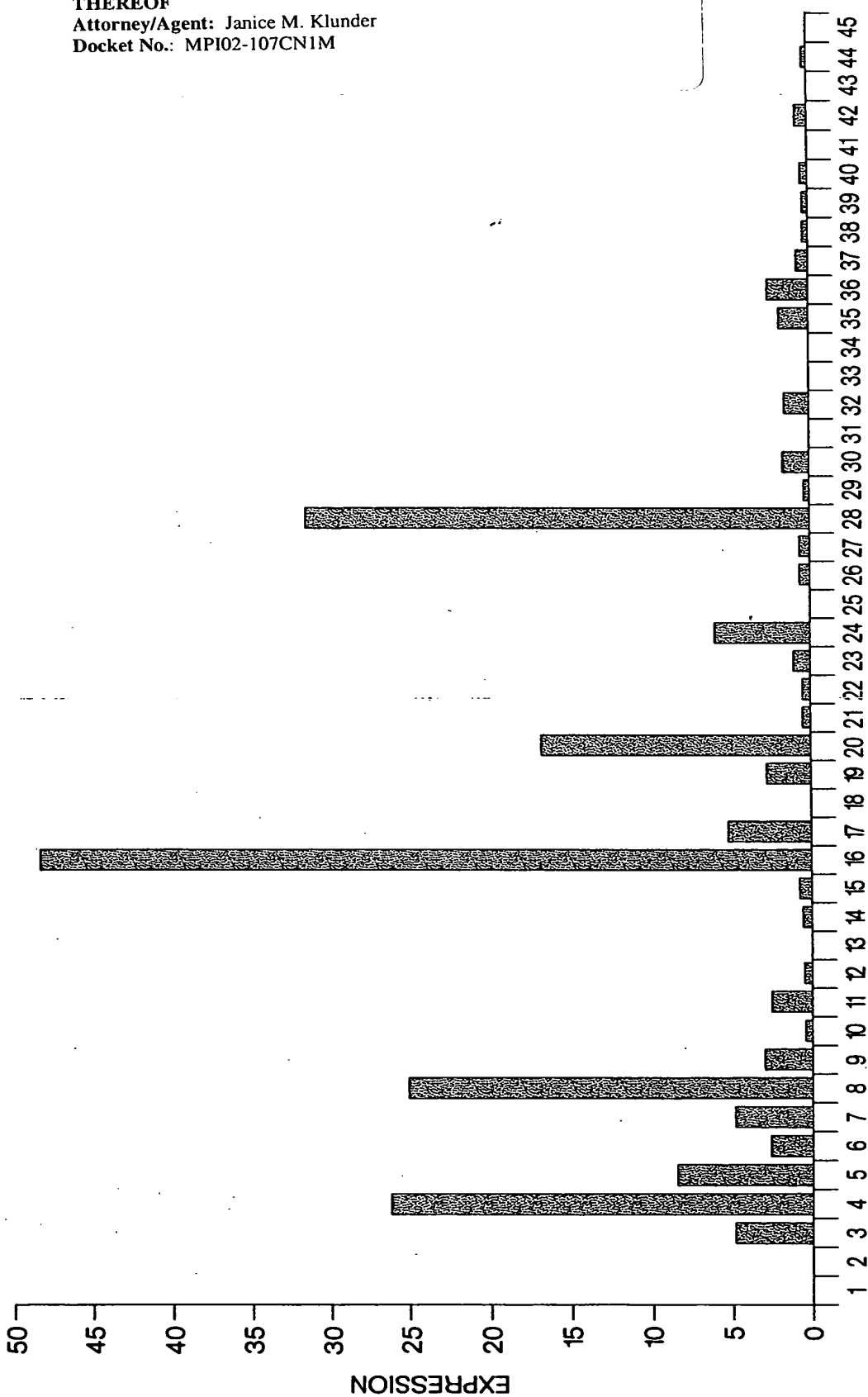


Fig. 11

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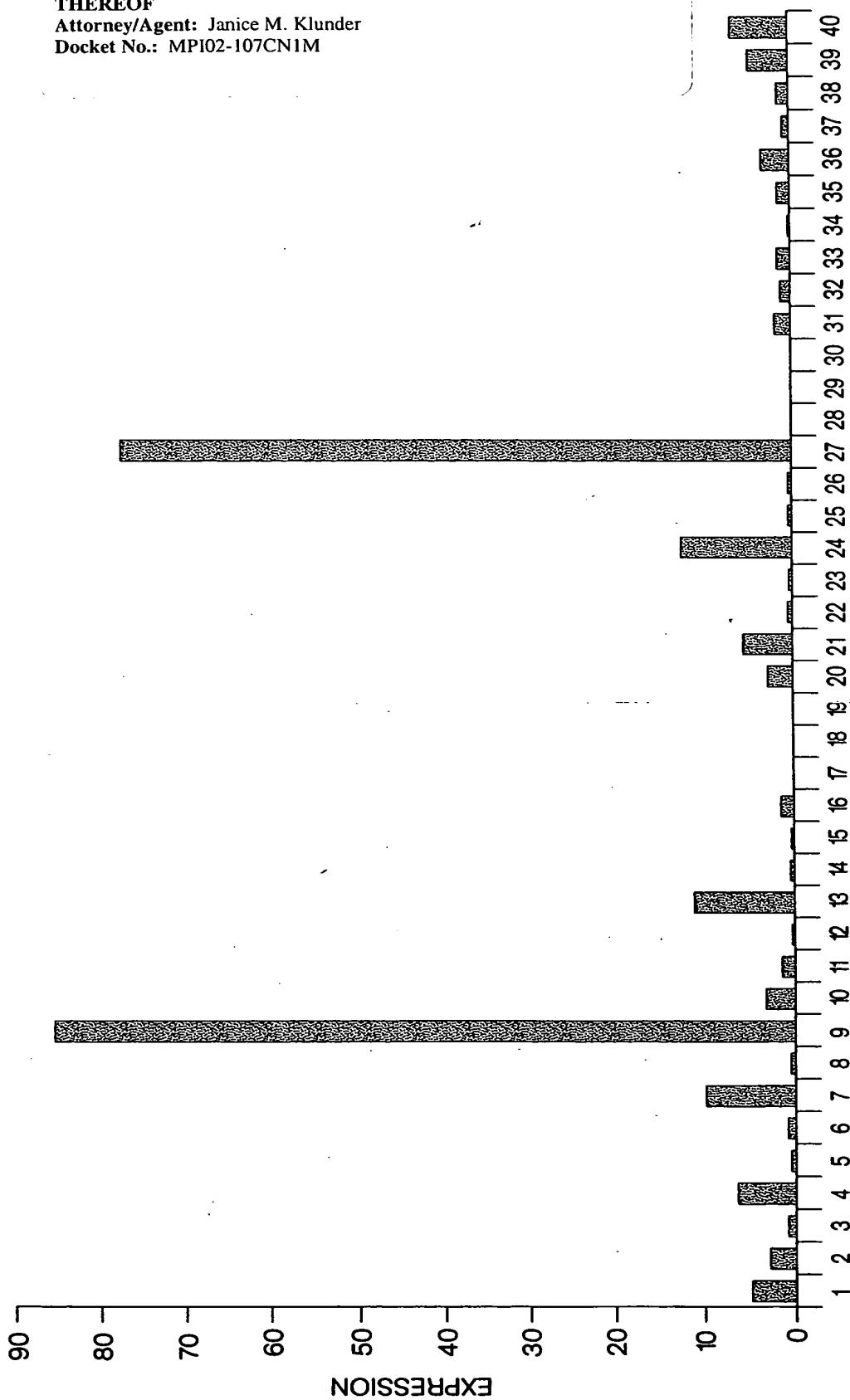


Fig. 12





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Docket No.: MPI02-107CN1M

Fbh 3370 FL. seq;

										M	A	G	T	N	T	L	L	M	L	10
CTCAGTCGTAAAGAGGAAAGGCAGAATTTTTCCTTGCT	ATG	GCT	GGA	ACA	AAC	ACA	CTT	TTG	ATG	CTG										30
E	N	F	I	D	G	K	F	L	P	C	S	S	Y	I	D	S	Y	D	P	30
GAA	AAC	TTC	ATA	GAT	GGA	AAA	TTT	TTA	CCT	TGT	AGC	TCA	TAT	ATA	GAT	TCT	TAC	GAC	CCA	90
S	T	G	E	V	Y	C	R	V	P	N	S	G	K	D	E	I	E	A	A	50
TCA	ACA	GGG	GAA	GTG	TAT	TGC	AGA	GTG	CCA	AAT	AGT	GGA	AAA	GAC	GAG	ATC	GAA	GCC	GCG	150
V	K	A	A	R	E	A	F	P	S	W	S	S	R	S	P	Q	E	R	S	70
GTC	AAG	GCC	GCC	AGA	GAA	GCC	TTT	CCC	AGC	TGG	TCA	TCC	CGC	AGC	CCC	CAG	GAG	CGC	TCA	210
R	V	L	N	Q	V	A	D	L	L	E	Q	S	L	E	E	F	A	Q	A	90
CGG	GTC	CTG	AAC	CAG	GTG	GCG	GAT	TTG	CTG	GAG	CAG	TCC	CTG	GAG	GAG	TTT	GCC	CAG	GCC	270
E	S	K	D	Q	G	K	T	L	A	L	A	R	T	M	D	I	P	R	S	110
GAG	TCT	AAA	GAC	CAA	GGG	AAA	ACC	TTA	GCA	CTG	GCA	AGA	ACC	ATG	GAC	ATT	CCC	CGG	TCT	330
V	Q	N	F	R	F	F	A	S	S	S	L	H	H	T	S	E	C	T	Q	130
GTG	CAG	AAC	TTC	AGG	TTC	TTC	GCT	TCC	TCC	AGC	CTG	CAC	CAC	ACG	TCA	GAG	TGC	ACG	CAG	390
M	D	H	L	G	C	M	H	Y	T	V	R	A	P	V	G	V	A	G	L	150
ATG	GAC	CAC	CTG	GGC	TGC	ATG	CAC	TAC	ACG	GTG	CGG	GCC	CCG	GTG	GGA	GTC	GCT	GGT	CTG	450
I	S	P	W	N	L	P	L	Y	L	L	T	W	K	I	A	P	A	M	A	170
ATC	AGC	CCC	TGG	AAT	TTG	CCA	CTC	TAC	TTG	CTG	ACC	TGG	AAG	ATA	GCT	CCA	GCG	ATG	GCT	510
A	G	N	T	V	I	A	K	P	S	E	L	T	S	V	T	A	W	M	L	190
GCA	GGG	AAC	ACT	GTG	ATA	GCC	AAG	CCC	AGT	GAG	CTG	ACT	TCA	GTG	ACT	GCG	TGG	ATG	TTG	570
C	K	L	L	D	K	A	G	V	P	P	G	V	V	N	I	V	F	G	T	210
TGC	AAA	CTC	CTG	GAT	AAA	GCA	GGT	GTT	CCA	CCA	GGT	GTG	GTC	AAT	ATT	GTG	TTT	GGA	ACC	630
G	P	R	V	G	E	A	L	V	S	H	P	E	V	P	L	I	S	F	T	230
GGG	CCC	AGG	GTG	GGT	GAG	GCC	CTG	GTG	TCC	CAC	CCA	GAG	GTG	CCC	CTG	ATC	TCC	TTC	ACC	690
G	S	Q	P	T	A	E	R	I	T	Q	L	S	A	P	H	C	K	K	L	250
GGG	AGC	CAG	CCC	ACC	GCT	GAG	CGG	ATC	ACC	CAG	CTG	AGC	GCT	CCC	CAC	TGC	AAA	AAG	CTC	750
S	L	E	L	G	G	K	N	P	A	I	I	F	E	D	A	N	L	D	E	270
TCC	CTG	GAG	CTG	GGG	GGC	AAG	AAT	CCT	GCC	ATC	ATC	TTT	GAG	GAC	GCC	AAC	CTG	GAT	GAG	810
C	I	P	A	T	V	R	S	S	F	A	N	Q	G	E	I	C	L	C	T	290
TGC	ATT	CCG	GCA	ACC	GTC	AGG	TCC	AGC	TTT	GCC	AAC	CAG	GGT	GAA	ATC	TGT	CTC	TGT	ACC	870
S	R	I	F	V	Q	K	S	I	Y	S	E	F	L	K	R	F	V	E	A	310
AGC	AGG	ATC	TTT	GTC	CAG	AAG	AGC	ATC	TAT	AGT	GAA	TTT	TTA	AAG	AGA	TTT	GTA	GAA	GCT	930
T	R	K	W	K	V	G	I	P	S	D	P	L	V	S	I	G	A	L	I	330
ACC	AGA	AAG	TGG	AAA	GTC	GGC	ATT	CCC	TCT	GAT	CCA	CTG	GTG	AGC	ATA	GGT	GCT	CTG	ATA	990
S	K	A	H	L	E	K	V	R	S	Y	V	K	R	A	L	A	E	G	A	350
AGT	AAA	GCA	CAT	TTG	GAG	AAA	GTC	AGA	AGT	TAC	GTC	AAG	AGA	GCT	CTT	GCT	GAA	GGT	GCC	1050

Fig. 14A

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

Q I W C G E G V D K L S L P A R N Q A G 370  
 CAA ATT TGG TGC GGT GAG GGA GTG GAT AAG TTG AGC CTC CCT GCC AGG AAC CAG GCA GGC 1110  
  
 Y F M L P T V I T D I K D E S C C M T E 390  
 TAC TTT ATG CTT CCC ACG GTG ATA ACA GAC ATT AAG GAT GAA TCC TGC TGC ATG ACG GAA 1170  
  
 E I F G P V T C V V P F D S E E E V I E 410  
 GAG ATA TTT GGT CCA GTG ACG TGT GTC GTC CCC TTT GAT AGT GAA GAG GAG GTG ATT GAA 1230  
  
 R A N N V K Y G L G A T V W S S N V G R 430  
 AGA GCC AAC AAC GTT AAG TAT GGG CTG GGG GCT ACC GTG TGG TCC AGC AAT GTG GGG CGC 1290  
  
 V H R V A K K L Q S G L V W T N C W L I 450  
 GTC CAC CGG GTG GCT AAG AAG CTG CAG TCT GGC TTG GTC TGG ACC AAC TGC TGG CTC ATC 1350  
  
 R E L N L P F G G M K S S G I G R E G A 470  
 AGG GAG CTG AAC CTT CCT TTC GGG GGG ATG AAG AGT TCT GGA ATA GGT AGA GAG GGA GCC 1410  
  
 K D S Y D F F T E I K T I T V K H \* 488  
 AAG GAC TCT TAC GAC TTC TTC ACT GAG ATC AAA ACC ATC ACC GTT AAA CAC TGA 1464  
  
 TCTTTGCTAATGGTGGAGCCACTATGGCCAATGCCTGGCTGCAGGCATCAGTTGTTCAATGTGGTAGATGAAAATCATG  
 GCATGAATTCCAGCTATGCCTTGACTTGGCAGAAGGTTATCTCTAGCTTATCCTCAGTTCTTAGTAACCTTTACCCACTA  
 GTGAAGAGATACTGTCTATTTTCAATGTGGACTCGGAAAAAAGACTTATAAGTAGGAAGATAGAACAATGATGCCAGT  
 TGTCAGGCTCCTCCCAGGTTATGTTTTCATAGTGTTCCTTTCATCATCTTCATTGAACTCTTGGGAATCTCCAGATAAT  
 CAGATTATTTTCAATTTGGTAAATTTTAAAAAATATGCAATCAGGCACAGTGCCTCATGCCTATAATCCCAGCACTTTGGG  
 AGGCCAAGGTGGGTGGATCACTTGAGTTCAGGAGTTCGAGATCAGCCTAGGCAACATGGTGAAATCCTGTCTTTACCAA  
 AAGTTTAAAAATTAGCTTGGTGTGGTGCCCTCTGCCTATAGCCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATCGCTT  
 GAGCCCAGCGGTTGAGGCTGCAGTGAGCCATGATCATTCCACTGCATTTTCAGCCTGGGGGATACAGTGAGACCTTGTC  
 TTTAAAAA

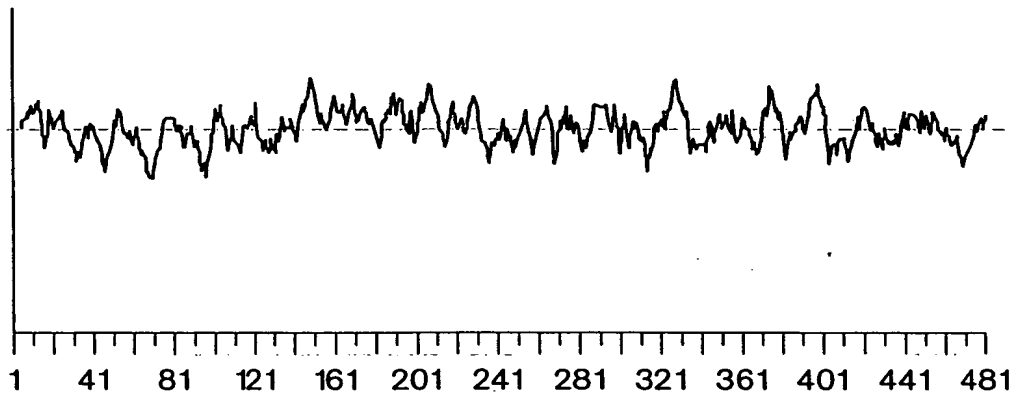
Fig. 14B

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M



>33770

MAGTNTLLMLENFIDGKFLPCSSYIDSYDPSTGEVYCRVPNSGKDEIEAAVKAAREAFPS  
WSSRSPQERSRVLNQVADLLEQSLEEFQAESKDQGKTLALARTMDIPRSVQNRFFASS  
SLHHTSECTQMDHLGCMHYTVRAPVGVAGLISPWNLPYLLTWKIAPAMAAGNTVIKPS  
ELTSVTAWMLCKLLDKAGVPPGVVNIVFGTGPRVGEALVSHPEVPLISFTGSQPTAERIT  
QLSAPHCKKLSLELGGKNPAIIFEDANLDECIPATVRSSFANQGEICLCTSRIFVQKSIY  
SEFLKRFVEATRKWKVGIPSDPLVSIGALISKAHLEKVRSYVKRRLAEGAQIWCGEVDK  
LSLPARNQAGYFMLPTVITDIKDESCMTEEIFGPVTCVVPFDSEEEVIERANNVKYGLG  
ATVWSSNVGRVHRVAKKLQSGLVWTNCWLIRELNLPGGMKSSGIGREGAKDSYDFFTEI  
KTITVKH

Fig. 15

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

## Alignments of top-scoring domains:

aldehyd: domain 1 of 1, from 17 to 487: score 656.6, E = 1.3e-193

```

      *->ewvdsasgktfevvnPankgevigrvpeataeDvdaAVkAAkeAfks
      ++ +      +++++P++ gev +rvp+++++++aAVkAA+eAf+s
33770   17   KFLPC--SSYIDSYDPST-GEVYCRVPNSGKDEIEAAVKAAREAFPS 60

      GpwWakvpaseRariLrkladlieeredelaaletdlGKplaeAkGdte
      wt +tt eR+r+L++ adl+et ++e+a +ettD+GK+la A ++
33770   61   ---WSSRSPQERSRVLNQVADLLEQSLEEFQAESKDQGKTIALART-MD 106

      vgraideiryyagwarklmgerrvipslatdgdeelnnytrrePlGVvgvI
      ++r +++++r++a      + +tt ++ ++ +      + yt+r P+GV g I
33770  107   IPRSVQNFRRFFASSSL--HHTSECTQMDHLG---CMHYTVRAPVGAGLI 151

      sPWNFPlllalwklapALAAgNTVVlKPSEqTPltalillaelieeaGann
      sPWN Pl l++wk+apA+AAgNTV+ KPSE+T +ta l++l+++aG
33770  152   SPWNLPYLLTWKIAPAMAAGNTVIAKPSELTSVTAWMLCKLLDKAG--- 198

      lPkGVvnvvpGfGaevGqaLkshpdlidlisFTGSteVGklimeaaAaknl
      +P+GVvn+ v G G+ vG aL+shp + isFTGS+++ + i +      a +
33770  199   VPPGVVNIVFGTGPRVGEALVSHPEVPLISFTGSQPTAERITQ-LSAPHC 247

      kkVtLELGgKsPvIVfdDADLdkAverivfgaFgnaGQvCiApsRllVhe
      kk +LELGgK+P I+f+DA+Ld ++ ++v++ F n+G++C ++sR++V++
33770  248   KKLSLELGgKNPAIIFEDANLDECIPATVRSSFANQGEICLCTSRIFVQK 297

      siydeFveklkervkkkliGdpldsdtniyGPlIseqqfdrvlslYedg
      siy eF+++ +ett k+k +G p dt ++i G+lIs+++++v sy++++
33770  298   SIYSEFLKRFVEATRKKW-VGIPSDPLVSI-GALISKAHLEKVRSYVKRA 345

      keeGakvlcG.Gerdeskeylgg.GyyvqPTiftdVtpdMkImkEEIFGP
      +eGA++ cG+G      s++ ++ Gy+ PT++td+++++ +m EEIFGP
33770  346   LAEGAQIWCGeGVDKLSLPARNQaGYFMLPTVITDIKDESCMTEEIFGP 395

      VlpiikfkdldeAIelaNdtEYGLAayvFTkdilarafrvakaleaGiVw
      V +++ f++++E+Ie+aN+++YGL+a v++++      r++rvak+l++G Vw
33770  396   VTCVVPFDSEEEVIERANNVKGGLGATVWSSN-VGRVHRVAKKLQSGLVW 444

      vNDvcvhaaepqlPFGGvKqSSGiGrehgGkygleeYteiKtVtirl<-*
      N c+ + e +lPFGG+K SGiGret k++ +++teiKt+t+++
33770  445   TN--CWLIRELNLPFGGMKS-SGIGREG-AKDSYDFFTEIKTITVKH 487

```

Fig. 16

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

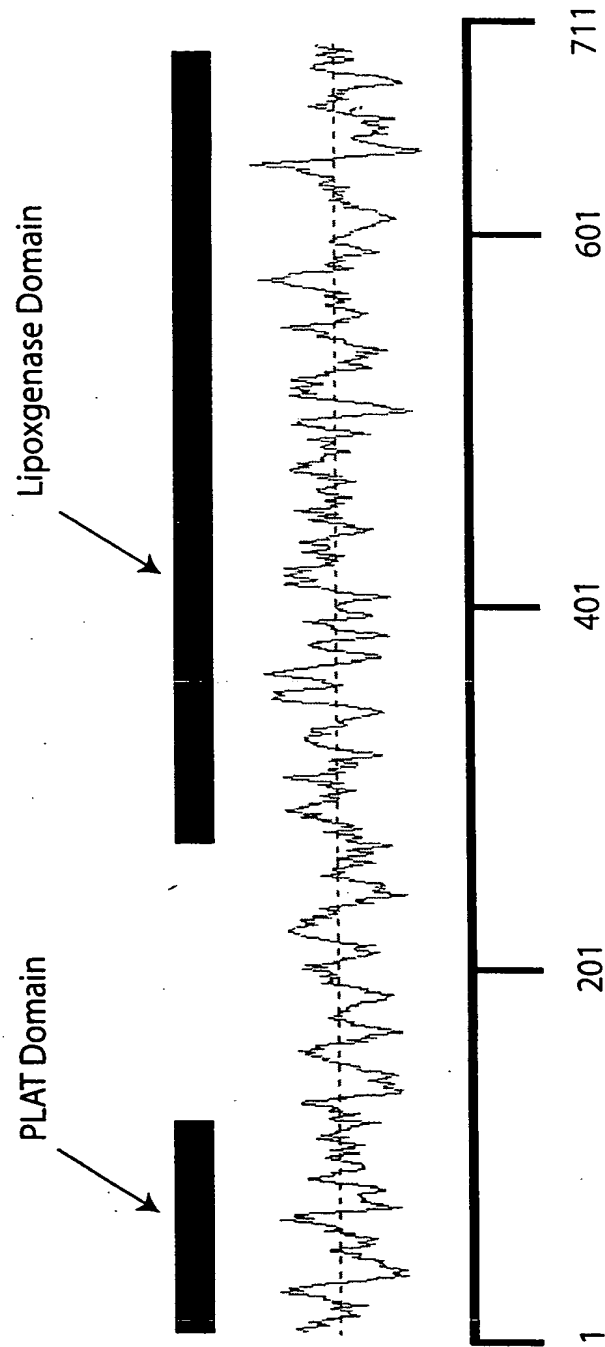


Fig. 17

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

**lipoxigenase: domain 1 of 1, from 267-703: score 480.2, E=1.7e-140**

```

*->aWmtDeeFAREmLAGvNPvvIrrlqeFPpkSKLDpavYGDqtStITk
      +W +D +F+++ L+GvNPv++ ++ ++P+k          +++T
46638 267   HWCEDHFFGYQYLYNGVNPVMLHCISLPSK-----LPVTN 301

      ehLElnL.gglTVeeAlqngrLFilDhhDlfiPylnkInsltstklYAtR
      +++ + L+  ++ +l+ g++F +D+ l  + n  +++ +A++
46638 302 DMVAPLLgQDTClQTELErGNIFLADYWILAEAPThCLN-GRQQYVAAPL 350

      TlFLkDgtLkPlAieLslPhpdgdpfGavskVflPadeGvessiWLLA
      +lL L++ g L+PlAI+Ls + p+ d  s++flP+d  ++WLLA
46638 351 CLLWLSPOGALVPLAIQLS-QTPGPD-----SPIFLPTDS---EWDWLLA 391

      KayVrvnDsgyHQLiSHWLnTHavvEPFvIATnRqLSvlHPiYKLLlPHY
      K++Vr++ + +H+  +H L TH+  E F+ AT RqL+  HPiYKLLlPH
46638 392 KTWVRNSEFLVHENNTFLCTHLLCEAFAMATLRQLPLCHPIYKLLlPHT 441

      RdTMnINaLRqsLinagGiEktflpgkyGaveMssavykkdWvFtdqA
      R+T+  N+ AR +L n +G+ ++  + g+ G + + s  + + ++t ++
46638 442 RYTLQVNTIARATLLNPEGLVDQVTSIGRQGLIYLMSTGLA-HFTYTNFC 490

      LPaDLvkRGlaveDpssPhGvRllIedYPYAvDGLeiWdaIktWVqeyVs
      LP+ L +RG++          I+ Y Y++DGL iW+aI+++V e+v
46638 491 LPDSLARGVLA-----IPNYHYRDDGLKIWAAlESFVSEIVG 528

```

**Fig. 18A**

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

```

1YYksDeavkkDpELQaWWkEvrevGHGDKDepWWpklgtredLievCT
YY+sD++v++D+ELQaW E+ ++ ++++++ 1 t+ + +++++T
46638 529 YYYPsDASVQDSELQaWTGEIFAQaFLGREGSGFPsRLCTPGEMVKFLT 578

iiIWiaSA1HAAVNFGQYpYgYipNRPttsRrPmPeegpvDtaeyeela
ii+ +SA+HAAVN GQ ++g++ pN+p+ +R+p+P +++
46638 579 AIIFNCSAQHAAVNSGQHDFGAWMPNAPSSMRQPPQTKG----- 618

knpekallkTitsqlqalldlsvieiLSrHasDEvYLGqrdepeWtsdkk
+ + k++l+T++ + ++ 1 +++++ S+ D +LG ++ e++++
46638 619 TTTLKTYLDTLPEVNISCNNLLLFWLVSQEPKQRPGLGTYPD-EHFTTEA 667

aleAFkrFgkkLaeIEkkIterNkDesLkNRvGpvklPYtLLkPs<-* (SEQ ID NO:25)
+ + F +La I I eRN + L lPYt+L P
46638 668 PRRSIAAFQSRLAQISRDIQERN--QGLA-----LPYTYLDPP 703

```

Fig. 18B

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

Alignments of top-scoring domains:

PLAT: domain 1 of 1, from 2 to 116: score 95.3, E = 1.2e-24

```

*->vsyqlivatgddstfagttgkvgislyGekgeskkikllkgelknlp
      + y+l v+tg      agt + +++ l+G+ ges+k+ l+++++
46638      2      AVYRLCVTTGP-YLRAGTLDNISVTLVGTCGESPKQRLDRMGR---- 43

      tlgfpggstfsfcdvdedfGelgavkiknehhslnsnptddewflksit
      +f+pgs+ ++++ + ++Gel+++++++e + + +++d w+++++i
46638      44 --DFAPGSVQKYKVRCTAELGELLRLRVHKERYAF---FRKDSWYCSRIC 88

      vedpqtqgevhFpcnsWvygktpkeylslic<-* (SEQ ID NO:26)
      v+ p++ + hFpc++W++g ++++ lr++
46638      89 VTEPDG-SVSHFPCYQWIEG---YCTVELRPG 116

```

Fig. 19A



Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

# Alignments of top-scoring domains:

LH2\_4: domain 1 of 1, from 2 to 116: score 80.9, E = 2.7e-20

\*->akykvtVtlgkKNvldfagttalgsllDgltldllGrqsvslsLiGae

46638 2 aY+ +Vt+g agt + ++s+ L+G+  
AVYRLCVTTG---PYLRAGTLD-----NISVTLVGTC 30

gddntgrgkesklaylerlTtlpslfargstye fefdvdedfGelgavk

46638 31 +es ++ l r++ ++fa+gs++ + + + +Gel+ +  
-----GESPKQRLDRMG----RDFAPGSVQKYKVRCTAELGELLRLR 68

iknehylfwssprhsefLksitlkdLgptggkvhFpCnswVypk kkp

46638 69 +++e+y+++f r++ ++++++i + + +g++ hFpC++W+ ++  
VHKERYAFF----RKDSWYCSRICVTEP--DGSVSHFPCYQWIEGY---- 108

ykgkriFfan<-\* (SEQ ID NO:27)

46638 109 + ++++++  
--CTVELRPG 116

Fig. 19B

Applicant: Rachel E. Meyers, et al.

Title: NOVE HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

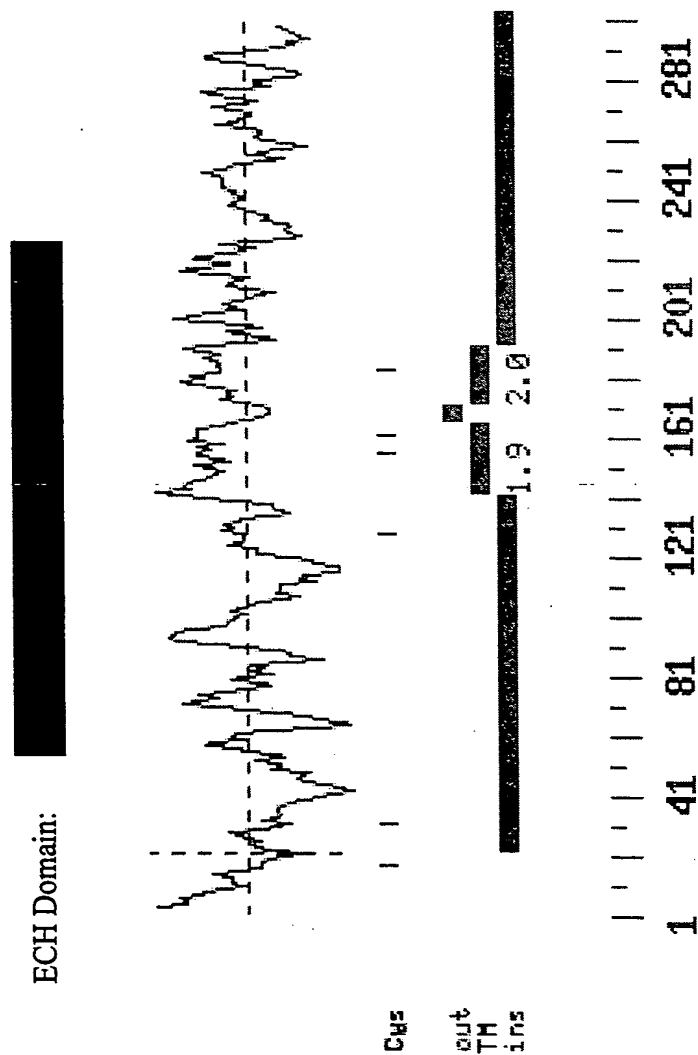


Fig. 20

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

**ECH: domain 1 of 1, from 57 to 225: score 143.2, E = 4.6e-39**

```

*->avikldrPeeavNalsae11tEl.ieAlekleqDpsvraVltGagp
      i+l +P+ + N+ls ++l +l+++ + ++++++++ + +
50090      57      RNIVLSNPK-KRNTLSLAMLKSLQSDILHDADSN-DLKVIIISAE-G 100

      gaFsaGaDikemaagfkeplaeqaqfsleaqdlwskledlpkPViAAVNG
      +Fs+G D+ke+++ + + a+ ++ ++ ++++++ p+PViA+VNG
50090      101 PVFSSGHDLKELTE--EQGRDYHAEVFQTCskVMMHIRNHPVPVIAMVNG 148

      yAlGGlelAlaLacDyrIAadnAkyvfglpEvklGiiPGaGGtqrLpRivG
      A ++G+ l+ +c +++A+d+++ f++p+v++G++ + + L+R+v+
50090      149 LATAAGCQLVASCNIaVAsDKSS--FATPGVNVGLFC-STPGVALARAVP 195

      vsaAlemiltGrriRAqEA1kmGlVdkVVp<-* (SEQ ID NO:31)
      ++ Alem+ tG++i+AqEAl +Gl +kVVp
50090      196 RKVALEMLFTGEPIsAQEALLHGLLSKVVP 225

```

**Fig. 21**